SEQUENCE LISTING

<110> The Scripps Research Institute et al.

<120> METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
      ANGIOGENESIS USING TYROSINE KINASE SRC

<130> TSRI 651.1

<140> Not yet known
<141> To be determined

<150> 60/087,220
<151> 1998-05-29

<160> 6

<170> PatentIn Ver. 2.0

<210> 1
<211> 11627
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:RCASBP(A) based
      on avian sarcoma virus

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<222> (7649)..(11258)
<223> pBR322 sequences

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<222> (7166)..(7494)
<223> upstream

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<222> (1)..(101)
<223> upstream (numbering begins at the upstream R)

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<222> (11394)..(11623)
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<221> misc_feature
<222> (388)..(391)
<223> splice donor (AGGT)

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<221> misc_feature
<222> (5074)..(5077)
<223> env splice acceptor (AGGC)

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<221> misc_feature
<222> (6982)..(6985)
<223> ClaI splice acceptor (AGGA)

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<222> (372)..(902)
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<222> (909)..(1094)
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<222> (1095)..(1814)
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<222> (2481)..(2483)
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<222> (4217)..(5185)
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<222> (5244)..(6263)
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<222> (6264)..(6878)
<223> env gp37

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<222> (6879)..(6881)
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<222> (7027)
<223> ClaI site/ the ClaI site in gag is methylated in
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gcattgcaga gatattgtat ttaagtgcct agctcgatac aataaac                11627


<210> 2
<211> 1759
<212> DNA
<213> Chicken

<220>
<221> gene
<222> (1)..(1759)
<223> chicken c-SRC cDNA

<220>
<221> CDS
<222> (112)..(1710)

<400> 2
 tctgacaccc atctgtctgt ctgtctgtgt gctgcaggag ctgagctgac tctgctgtgg 60

 cctcgcgtac cactgtggcc aggcggtagc tgggacgtgc agcccaccac c atg ggg  117
```

```
                                                                Met Gly
                                                                 1

agc agc aag agc aag ccc aag gac ccc agc cag cgc cgg cgc agc ctg    165
Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg Arg Arg Ser Leu
            5             10              15

gag cca ccc gac agc acc cac cac ggg gga ttc cca gcc tcg cag acc    213
Glu Pro Pro Asp Ser Thr His His Gly Gly Phe Pro Ala Ser Gln Thr
        20              25              30

ccc aac aag aca gca gcc ccc gac acg cac cgc acc ccc agc cgc tcc    261
Pro Asn Lys Thr Ala Ala Pro Asp Thr His Arg Thr Pro Ser Arg Ser
35              40              45              50

ttt ggg acc gtg gcc acc gag ccc aag ctc ttc ggg ggc ttc aac act    309
Phe Gly Thr Val Ala Thr Glu Pro Lys Leu Phe Gly Gly Phe Asn Thr
                55              60              65

tct gac acc gtt acg tcg ccg cag cgt gcc ggg gca ctg gct ggc ggc    357
Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Ala Leu Ala Gly Gly
            70              75              80

gtc acc act ttc gtg gct ctc tac gac tac gag tcc cgg act gaa acg    405
Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser Arg Thr Glu Thr
            85              90              95

gac ttg tcc ttc aag aaa gga gaa cgc ctg cag att gtc aac aac acg    453
Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile Val Asn Asn Thr
        100             105             110

gaa ggt gac tgg tgg ctg gct cat tcc ctc act aca gga cag acg ggc    501
Glu Gly Asp Trp Trp Leu Ala His Ser Leu Thr Thr Gly Gln Thr Gly
115             120             125             130

tac atc ccc agt aac tat gtc gcg ccc tca gac tcc atc cag gct gaa    549
Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp Ser Ile Gln Ala Glu
                135             140             145

gag tgg tac ttt ggg aag atc act cgt cgg gag tcc gag cgg ctg ctg    597
Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg Leu Leu
            150             155             160

ctc aac ccc gaa aac ccc cgg gga acc ttc ttg gtc cgg gag agc gag    645
Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu Ser Glu
        165             170             175

acg aca aaa ggt gcc tat tgc ctc tcc gtt tct gac ttt gac aac gcc    693
Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Asp Asn Ala
        180             185             190

aag ggg ctc aat gtg aag cac tac aag atc cgc aag ctg gac agc ggc    741
Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp Ser Gly
195             200             205             210

ggc ttc tac atc acc tca cgc aca cag ttc agc agc ctg cag cag ctg    789
Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu Gln Gln Leu
                215             220             225

gtg gcc tac tac tcc aaa cat gct gat ggc ttg tgc cac cgc ctg acc    837
Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His Arg Leu Thr
                230             235             240

aac gtc tgc ccc acg tcc aag ccc cag acc cag gga ctc gcc aag gac    885
```

```
Asn Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp
        245                 250                 255

gcg tgg gaa atc ccc cgg gag tcg ctg cgg ctg gag gtg aag ctg ggg      933
Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly
    260                 265                 270

cag ggc tgc ttt gga gag gtc tgg atg ggg acc tgg aac ggc acc acc      981
Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr
275                 280                 285                 290

aga gtg gcc ata aag act ctg aag ccc ggc acc atg tcc ccg gag gcc     1029
Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Glu Ala
                295                 300                 305

ttc ctg cag gaa gcc caa gtg atg aag aag ctc cgg cat gag aag ctg     1077
Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu Lys Leu
                310                 315                 320

gtt cag ctg tac gca gtg gtg tcg gaa gag ccc atc tac atc gtc act     1125
Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr
            325                 330                 335

gag tac atg agc aag ggg agc ctc ctg gat ttc ctg aag gga gag atg     1173
Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly Glu Met
    340                 345                 350

ggc aag tac ctg cgg ctg cca cag ctc gtc gat atg gct gct cag att     1221
Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile
355                 360                 365                 370

gca tcc ggc atg gcc tat gtg gag agg atg aac tac gtg cac cga gac     1269
Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His Arg Asp
                375                 380                 385

ctg cgg gcg gcc aac atc ctg gtg ggg gag aac ctg gtg tgc aag gtg     1317
Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Val
                390                 395                 400

gct gac ttt ggg ctg gca cgc ctc atc gag gac aac gag tac aca gca     1365
Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala
            405                 410                 415

cgg caa ggt gcc aag ttc ccc atc aag tgg aca gcc ccc gag gca gcc     1413
Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala
    420                 425                 430

ctc tat ggc cgg ttc acc atc aag tcg gat gtc tgg tcc ttc ggc atc     1461
Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile
435                 440                 445                 450

ctg ctg act gag ctg acc acc aag ggc cgg gtg cca tac cca ggg atg     1509
Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro Gly Met
                455                 460                 465

gtc aac agg gag gtg ctg gac cag gtg gag agg ggc tac cgc atg ccc     1557
Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg Met Pro
                470                 475                 480

tgc ccg ccc gag tgc ccc gag tcg ctg cat gac ctc atg tgc cag tgc     1605
Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys Gln Cys
            485                 490                 495

tgg cgg agg gac cct gag gag cgg ccc act ttt gag tac ctg cag gcc     1653
```

```
    Trp Arg Arg Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ala
        500             505             510

    ttc ctg gag gac tac ttc acc tcg aca gag ccc cag tac cag cct gga   1701
    Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln Tyr Gln Pro Gly
    515             520             525             530

    gag aac cta taggcctgga gctcctcctg gaccagaggc ctcgctgtgg ggtacaggg  1759
    Glu Asn Leu
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<210> 3
<211> 533
<212> PRT
<213> Chicken

<400> 3
    Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg Arg Arg
    1               5               10              15

    Ser Leu Glu Pro Pro Asp Ser Thr His His Gly Gly Phe Pro Ala Ser
                20              25              30

    Gln Thr Pro Asn Lys Thr Ala Ala Pro Asp Thr His Arg Thr Pro Ser
            35              40              45

    Arg Ser Phe Gly Thr Val Ala Thr Glu Pro Lys Leu Phe Gly Gly Phe
        50              55              60

    Asn Thr Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Ala Leu Ala
    65              70              75              80

    Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser Arg Thr
                85              90              95

    Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile Val Asn
                100             105             110

    Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Thr Thr Gly Gln
                115             120             125

    Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp Ser Ile Gln
        130             135             140

    Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg
    145             150             155             160

    Leu Leu Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu
                165             170             175

    Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Asp
                180             185             190

    Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp
                195             200             205

    Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu Gln
        210             215             220

    Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His Arg
    225             230             235             240

    Leu Thr Asn Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly Leu Ala
                245             250             255
```

```
Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys
            260             265             270

Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly
            275             280             285

Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro
    290             295             300

Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu
305             310             315             320

Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile
            325             330             335

Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly
            340             345             350

Glu Met Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala
            355             360             365

Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His
    370             375             380

Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys
385             390             395             400

Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr
            405             410             415

Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu
            420             425             430

Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe
            435             440             445

Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro
    450             455             460

Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg
465             470             475             480

Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys
            485             490             495

Gln Cys Trp Arg Arg Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu
            500             505             510

Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln Tyr Gln
            515             520             525

Pro Gly Glu Asn Leu
    530
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<210> 4
<211> 2187
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (1)..(2187)
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<223> human c-SRC cDNA

<220>
<221> CDS
<222> (134)..(1483)

<400> 4
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caagagagct ctaatggtac caagtgacag gttggcttta ctgtgactcg gggacgccag 120

agctcctgag aag atg tca gca ata cag gcc gcc tgg cca tcc ggt aca   169
            Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr
            1   5   10

gaa tgt att gcc aag tac aac ttc cac ggc act gcc gag cag gac ctg   217
Glu Cys Ile Ala Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu
        15   20   25

ccc ttc tgc aaa gga gac gtg ctc acc att gtg gcc gtc acc aag gac   265
Pro Phe Cys Lys Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp
        30   35   40

ccc aac tgg tac aaa gcc aaa aac aag gtg ggc cgt gag ggc atc atc   313
Pro Asn Trp Tyr Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile
45   50   55   60

cca gcc aac tac gtc cag aag cgg gag ggc gtg aag gcg ggt acc aaa   361
Pro Ala Asn Tyr Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys
                65   70   75

ctc agc ctc atg cct tgg ttc cac ggc aag atc aca cgg gag cag gct   409
Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala
                80   85   90

gag cgg ctt ctg tac ccg ccg gag aca ggc ctg ttc ctg gtg cgg gag   457
Glu Arg Leu Leu Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu
        95   100   105

agc acc aac tac ccc gga gac tac acg ctg tgc gtg agc tgc gac ggc   505
Ser Thr Asn Tyr Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly
        110   115   120

aag gtg gag cac tac cgc atc atg tac cat gcc agc aag ctc agc atc   553
Lys Val Glu His Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile
125   130   135   140

gac gag gag gtg tac ttt gag aac ctc atg cag ctg gtg gag cac tac   601
Asp Glu Glu Val Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr
                145   150   155

acc tca gac gca gat gga ctc tgt acg cgc ctc att aaa cca aag gtc   649
Thr Ser Asp Ala Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val
                160   165   170

atg gag ggc aca gtg gcg gcc cag gat gag ttc tac cgc agc ggc tgg   697
Met Glu Gly Thr Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp
                175   180   185

gcc ctg aac atg aag gag ctg aag ctg ctg cag acc atc ggg aag ggg   745
Ala Leu Asn Met Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly
        190   195   200

gag ttc gga gac gtg atg ctg ggc gat tac cga ggg aac aaa gtc gcc   793

```
Glu Phe Gly Asp Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala
205             210             215             220

gtc aag tgc att aag aac gac gcc act gcc cag gcc ttc ctg gct gaa    841
Val Lys Cys Ile Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu
                225             230             235

gcc tca gtc atg acg caa ctg cgg cat agc aac ctg gtg cag ctc ctg    889
Ala Ser Val Met Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu
                240             245             250

ggc gtg atc gt· gag gag aag ggc ggg ctc tac atc gtc act gag tac    937
Gly Val Ile Val Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr
                255             260             265

atg gcc aag ggg agc ctt gtg gac tac ctg cgg tct agg ggt cgg tca    985
Met Ala Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser
        270             275             280

gtg ctg ggc gga gac tgt ctc ctc aag ttc tcg cta gat gtc tgc gag   1033
Val Leu Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu
285             290             295             300

gcc atg gaa tac ctg gag ggc aac aat ttc gtg cat cga gac ctg gct   1081
Ala Met Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala
                305             310             315

gcc cgc aat gtg ctg gtg tct gag gac aac gtg gcc aag gtc agc gac   1129
Ala Arg Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp
                320             325             330

ttt ggt ctc acc aag gag gcg tcc agc acc cag gac acg ggc aag ctg   1177
Phe Gly Leu Thr Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu
        335             340             345

cca gtc aag tgg aca gcc cct gag gcc ctg aga gag aag aaa ttc tcc   1225
Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser
        350             355             360

act aag tct gac gtg tgg agt ttc gga atc ctt ctc tgg gaa atc tac   1273
Thr Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr
365             370             375             380

tcc ttt ggg cga gtg cct tat cca aga att ccc ctg aag gac gtc gtc   1321
Ser Phe Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val
                385             390             395

cct cgg gtg gag aag ggc tac aag atg gat gcc ccc gac ggc tgc ccg   1369
Pro Arg Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro
                400             405             410

ccc gca gtc tat gaa gtc atg aag aac tgc tgg cac ctg gac gcc gcc   1417
Pro Ala Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala
                415             420             425

atg cgg ccc tcc ttc cta cag ctc cga gag cag ctt gag cac atc aaa   1465
Met Arg Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys
        430             435             440

acc cac gag ctg cac ctg tgacggctgg cctccgcctg ggtcatgggc          1513
Thr His Glu Leu His Leu
445             450

ctgtggggac tgaacctgga agatcatgga cctggtgccc ctgctcactg ggcccgagcc 1573
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tgaactgagc cccagcgggc tggcgggcct ttttcctgcg tcccagcctg cacccctccg 1633

gccccgtctc tcttggaccc acctgtgggg cctggggagc ccactgaggg gccagggagg 1693

aaggaggcca cggagcggga ggcagcgccc caccacgtcg ggcttccctg gcctcccgcc 1753

actcgccttc ttagagtttt attcctttcc ttttttgaga ttttttttcc gtgtgtttat 1813

tttttattat ttttcaagat aaggagaaag aaagtaccca gcaaatgggc attttacaag 1873

aagtacgaat cttatttttc ctgtcctgcc cgtgagggtg gggggaccg ggccctctc 1933

tagggacccc tcgccccagc ctcattcccc attctgtgtc ccatgtcccg tgtctcctcg 1993

gtcgccccgt gtttgcgctt gaccatgttg cactgtttgc atgcgcccga ggcagacgtc 2053

tgtcaggggc ttggatttcg tgtgccgctg ccacccgccc accgccttg tgagatggaa 2113

ttgtaataaa ccacgccatg aggacaccgc cgcccgcctc ggcgcttcct ccaccgaaaa 2173

aaaaaaaaaa aaaa                                                     2187
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<210> 5
<211> 450
<212> PRT
<213> Homo sapiens

<400> 5
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Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
 1               5                  10                  15

Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
                20                  25                  30

Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
            35                  40                  45

Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
        50                  55                  60

Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
65                  70                  75                  80

Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
                85                  90                  95

Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
                100                 105                 110

Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
            115                 120                 125

Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
    130                 135                 140

Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
145                 150                 155                 160

Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
                165                 170                 175

Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
```

```
                    180                  185                  190
Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
        195                 200                 205

Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
        210                 215                 220

Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
225                 230                 235                 240

Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
                245                 250                 255

Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
                260                 265                 270

Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
                275                 280                 285

Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
    290                 295                 300

Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
305                 310                 315                 320

Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
                325                 330                 335

Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
                340                 345                 350

Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
                355                 360                 365

Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
    370                 375                 380

Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
385                 390                 395                 400

Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
                405                 410                 415

Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
                420                 425                 430

Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
                435                 440                 445

His Leu
    450
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<210> 6
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:9E10-myc
        epitope tag

<400> 6
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Val Asp Met Glu Gln Lys Leu Ile Ala Glu Glu Asp Leu Asn
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